**Figure 1. Effect of p21 (149-160) on CDK2-Cyclin E induced phopshorylation of different concentrations Histone 1. Yellow line (+)– 1mg/ml Histone1, purple line (diamonds), 0.7 mg/ml Histone 1, blue line (x)– 0.25 mg/ml Histone 1 and brown line (closed circles) – 0.1 mg/ml Histone 1.**

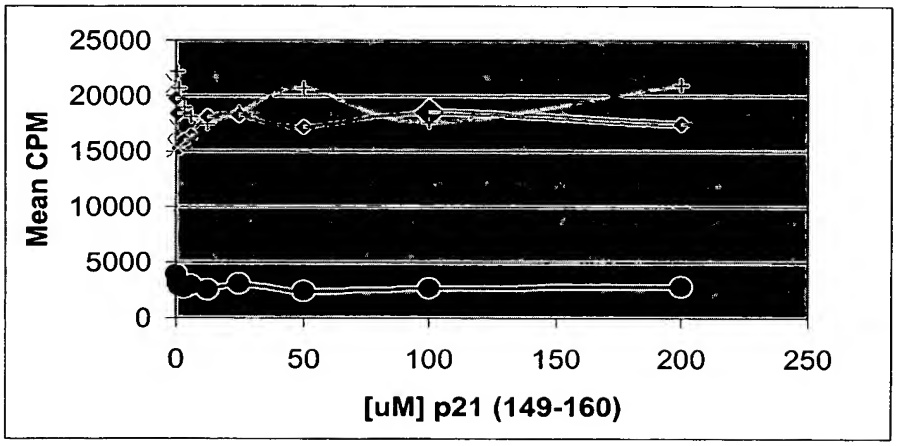
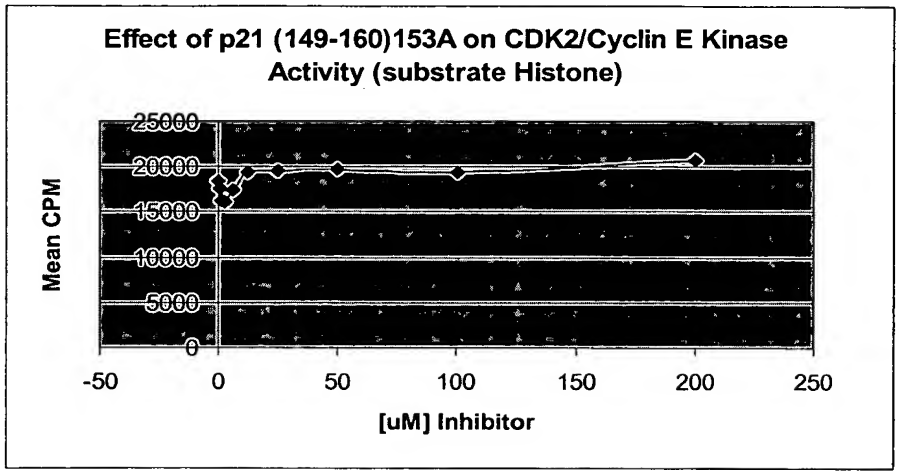
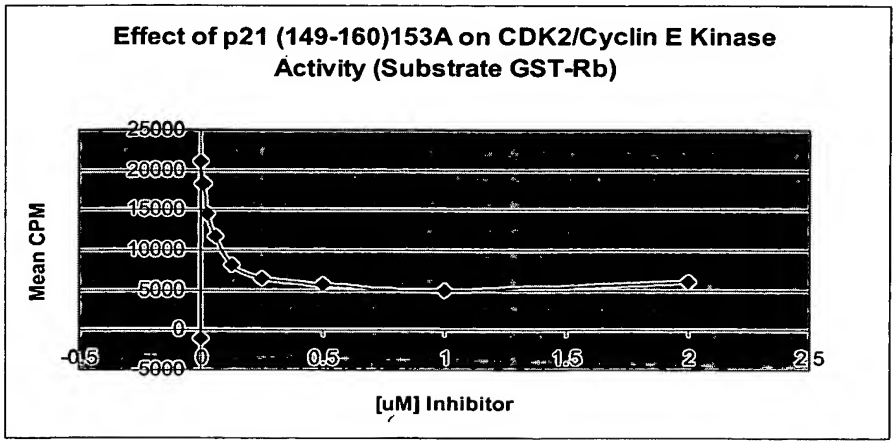


**Figure 2. p21 (141-160)153A is a strong inhibitor of GST-Rb phopshorylation but not of Histone 1 phosphorylation induced by CDK2-Cyclin E kinase complex.**



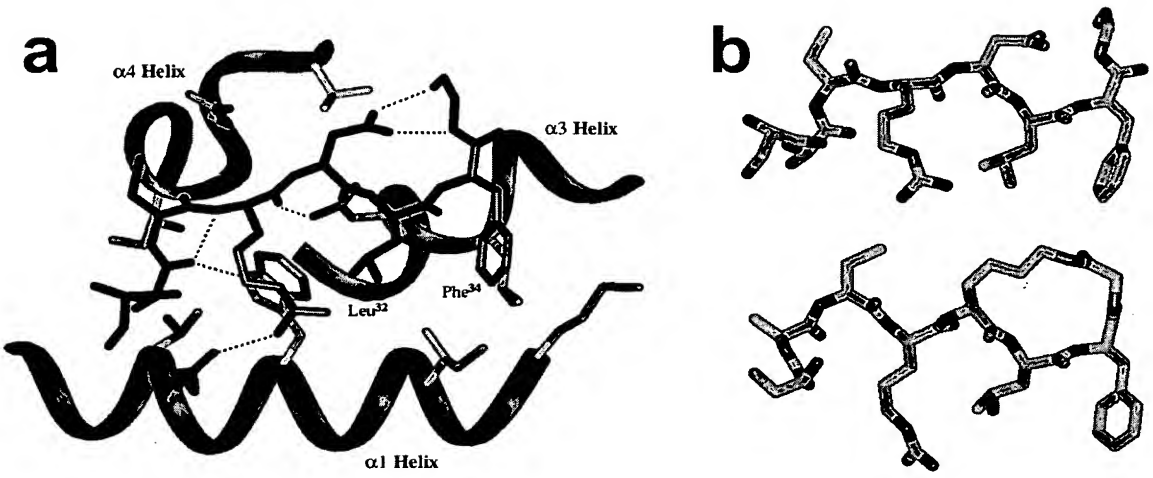



***Figure 3.***: . **a**: Interactions of p27($^{27}$Ser-Ala-Cys-Arg-Asn-Leu-Phe-Gly$^{34}$) segment with cyclin A groove (Russo, A. A.; Jeffrey, P. D.; Patten, A. K.; Massague, J.; Pavletich, N. P. *Nature* **1996**, *382*, 325-31).; **b**: conformation of the same segment (top) compared with modelled cyclic Ser-Ala-Cys-Arg-Lys-Leu-Phe-Gly peptide (bottom).

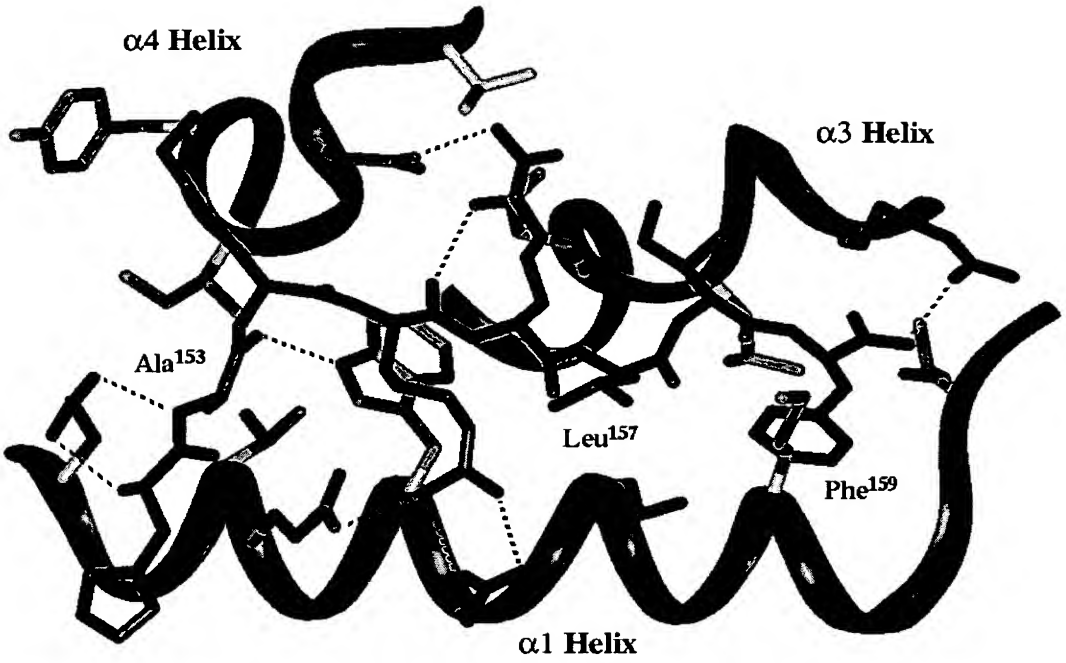



**Figure 4**. The 3-D structure of the peptide H-His-Ala-Lys-Arg-Arg-Leu-Ile-Phe-$NH_2$ / cyclin A complex was generated using molecular docking techniques. The peptide structure is represented in black, while only the residues of the cyclin groove that make intermolecular contacts with the peptide are shown. The backbone of cyclin A is represented by the grey ribbon.

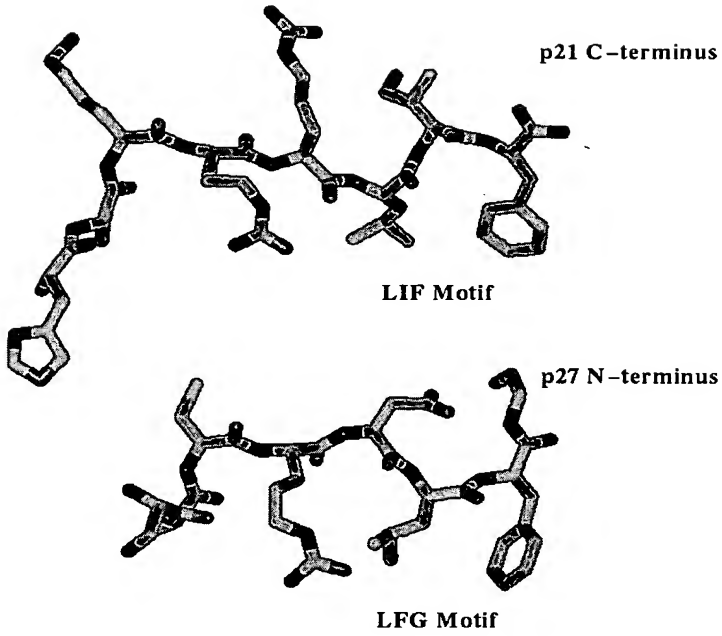



**Figure 5.** Comparison of the conformation of cyclin A-complexed structures of the p21- and p27-derived peptides H-His-Ala-Lys-Arg-Arg-Leu-Ile-Phe and H-Ser-Ala-Cys-Arg-Asn-Leu-Phe-Gly-$NH_2$. The positioning of the Leu and Phe side chains of the Leu-Ile-Phe and Leu-Phe-Gly motifs in the groove is remarkably similar, despite the different sequence order of these residues.

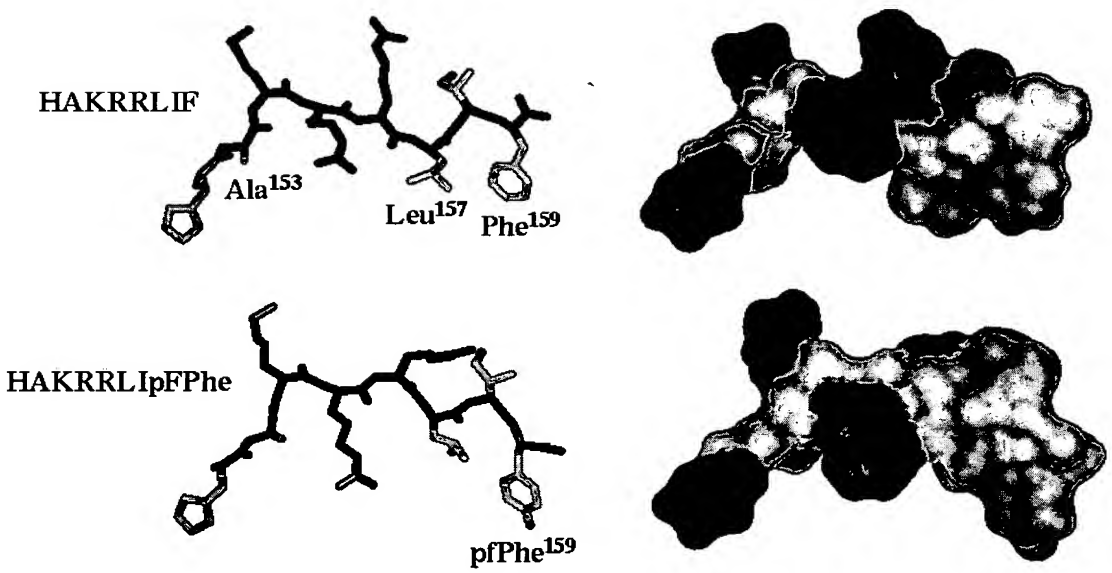



**Figure 6** Comparison of modelled cyclin A groove-bound conformations of the p21(152-159)Ser153Ala peptides containing either $Phe^{159}$ (top) or $pFPhe^{159}$ (bottom).